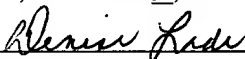




PATENT
Docket No. 220002060310

CERTIFICATE OF MAILING BY "FIRST CLASS MAIL"

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to:
Assistant Commissioner for Patents, Washington, D.C. 20231, on November 21, 2001.


Denise Lade

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the application of:

Shaun R. COUGHLIN et al.

Serial No.: 09/208,629

Filing Date: December 8, 1998

For: PROTEASE ACTIVATED RECEPTOR 3
AND USES THEREOF

Examiner: M. Pak

Group Art Unit: 1646

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TECH CENTER 1600/2900

**RESPONSE TO NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT
APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO
ACID SEQUENCE DISCLOSURES**

Box Sequence
Commissioner for Patents
Washington, D.C. 20231

Dear Sir:

This communication is in response to a "Notice to Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures" dated October 15, 2001.

Remarks

The printed Sequence Listing is identical to the Sequence Listing submitted in computer-readable form.

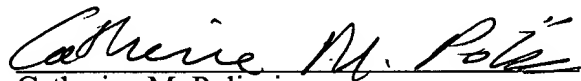
This paper is submitted to comply with the United States Patent Office rules governing gene sequences. No new matter is added by the submission of this sequence listing.

In the unlikely event that the fee transmittal is separated from this document and/or the U.S. Patent Office determines that an extension and/or other relief is required, applicants petition for any required relief including extensions of time and authorize the Assistant Commissioner to charge the cost of such petitions and/or other fees due in connection with the filing of this sequence listing to our **Deposit Account No. 03-1952**. However, the Assistant Commissioner is not authorized to charge the cost of the issue fee to the Deposit Account.

Respectfully submitted,

Dated: November 26, 2001

By:


Catherine M. Polizzi
Registration No. 40,130

Morrison & Foerster LLP
755 Page Mill Road
Palo Alto, California 94304-1018
Telephone: (650) 813-5651
Facsimile: (650) 494-0792



Application No.: 09/208,629

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

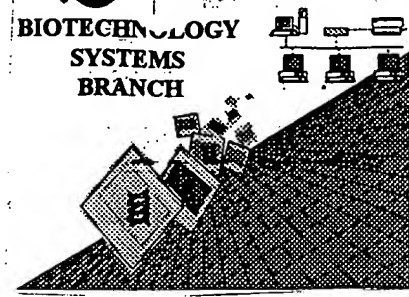
For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

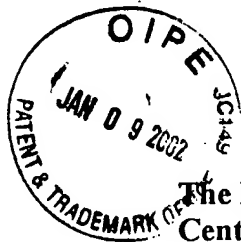
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RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/208,629
Source: 1646
Date Processed by STIC: 11/29/2000

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- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/208,629DATE: 12/10/2000
TIME: 03:01:30

INPUT SET: S36189.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

Does Not Comply
Corrected Diskette Needed

RECEIVED

TECH CENTER 160

(1) General Information

(i) APPLICANT: Coughlin, Shaun R.
Ishihari, Hiroaki
Connolly, Andrew

(ii) TITLE OF THE INVENTION: Protease-Activated Receptor
3 and Uses Thereof

(iii) NUMBER OF SEQUENCES: 23 p. 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: MORRISON & FOERSTER
(B) STREET: 755 Page Mill Road
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/208,629
(B) FILING DATE: 08-DEC-1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/742,440
(B) FILING DATE: 30-OCT-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Catherine M. Polizzi
(B) REGISTRATION NUMBER: 40,130
(C) REFERENCE/DOCKET NUMBER: 220002060310

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650) 813-5600
(B) TELEFAX: (650) 494-0792

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/208,629DATE: 12/10/2000
TIME: 03:01:30

INPUT SET: S36189.raw

47 (C) TELEX:

48

49

50 (2) INFORMATION FOR SEQ ID NO:1:

51

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 1224 base pairs

54 (B) TYPE: nucleic acid

55 (C) STRANDEDNESS: double

56 (D) TOPOLOGY: linear

57

58 (ii) MOLECULE TYPE: cDNA

59

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

61

62	TGACTTTGTA	TACTTAACAA	CATCCTGTAG	CCGGGTCTCA	GGACATCAAG	ATGAAAATCC	60
63	TTATCTTGGT	TGCAGCTGGG	CTGCTGTTTC	TGCCAGTCAC	TGTTTGCCAA	AGTGGCATAA	120
64	ATGTTTCAGA	CAACTCAGCA	AAGCCAACCT	TAACTATTAA	GAGTTTAAAT	GGGGGTCCCC	180
65	AAAATACCTT	TGAAGAATTC	CCACTTTCTG	ACATAGAGGG	CTGGACAGGA	GCCACCACAA	240
66	CTATAAAAGC	GGAGTGTCCT	GAGGACAGTA	TTTCAACTCT	CCACGTGAAT	AATGCTACCA	300
67	TAGGATACCT	GAGAAGTTCC	TTAAGTACCC	AAGTGATACC	TGCCATCTAT	ATCCTGCTGT	360
68	TTGTGGTTGG	TGTACCATCC	AACATCGTGA	CCCTGTGGAA	ACTCTCCTTA	AGGACCAAAT	420
69	CCATCAGTCT	GGTCATCTTT	CACACCAACC	TGGCCATCGC	AGATCTCCTT	TTCTGTGTCA	480
70	CACTGCCATT	TAAGATCGCC	TACCATCTCA	ATGGCAACAA	CTGGGTATTT	GGCGAGGTCA	540
71	TGTGCCGGAT	CACCACGGTC	GTTTTCTACG	GCAACATGTA	CTGCGCTATC	CTGATCCTCA	600
72	CTTGCAATGG	CATCAACCGC	TACCTGGCCA	CGGCTCACCC	TTTCACATAC	CAGAAGCTGC	660
73	CCAAACGCAG	CTTCTCCTTG	CTCATGTGTG	GCATAGTGTG	GGTCATGGTT	TTCTTATACA	720
74	TGCTGCCCTT	TGTCATCCTG	AAGCAGGAGT	ACCACCTCGT	CCACTCAGAG	ATCACCACCT	780
75	GCCACGATGT	CGTCGACGCG	TGCGAGTCCC	CATCATCCTT	CCGATTCTAC	TACTTCGTCT	840
76	CCTTAGCATT	CTTTGGGTTT	CTCATCCCCT	TTGTGATCAT	CATCTTCTGT	TACACGACTC	900
77	TCATCCACAA	ACTTAAATCA	AAGGATCGGA	TATGGCTGGG	CTACATCAAG	GCCGTCTCTC	960
78	TCATCCTTGT	GATTTTCACA	ATTTGCTTTG	CCCCACCAA	CATCATACTC	GTAATCCACC	1020
79	ATGCCAACTA	CTACTACCAC	AATACCGACA	GCTTGTAATT	TATGTATCTT	ATTGCTCTGT	1080
80	GCCTGGGGAG	CCTGAATAGC	TGCCTAGATC	CATTCCCTTA	CTTTGTTCATG	TCGAAAGTTG	1140
81	TAGATCAGCT	TAATCCTTAG	TCGGCAATGG	CAAGACCACT	TTAGAGACCA	AGGAGAGATA	1200
82	TCTGGGAAGA	CATACATGCT	TGGC				1224

83

84 (2) INFORMATION FOR SEQ ID NO:2:

85

86 (i) SEQUENCE CHARACTERISTICS:

87 (A) LENGTH: 1124 base pairs

88 (B) TYPE: nucleic acid

89 (C) STRANDEDNESS: double

90 (D) TOPOLOGY: linear

91

92 (ii) MOLECULE TYPE: Genomic DNA

93 (ix) FEATURE:

94

95 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

96

97	CCATATGCTA	ATATTTCTCT	TCAATTACAG	GCATAAATGT	TTCAGACAAC	TCAGCAAAGC	60
98	CAACCTTAAC	TATTAAGAGT	TTTAATGGGG	GTCCCCAAAA	TACCTTTGAA	GAATTCNNNN	120
99	NNNTACAAC	CTCCATGTGA	ATAATGCTAC	CATGGGATAC	CTGAGAAGTT	CCTTAAGTAC	180

RAW SEQUENCE LISTING PATENT APPLICATION US/09/208,629

TECH CENTER 1600/2900 DATE: 12/10/2000
TIME: 03:01:30

INPUT SET: S36189.raw

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100 CAAAGTGATA CCTGCCATCT ACATCCTGGT GTTTGTGATT GGTGTACCAG CGAACATCGT 240
101 GACCCTGTGG AAACCTCTCT CAAGGACCAA ATCCATCTGT CTGGTCATCT TTCACACCAA 300
102 CCTGGCCATC GCGGATCTCC TTTTCTGTGT CACGCTGCCG TTTAAGATCN NCCTACCATC 360
103 TCAATGGCAA CAACTGGGTA TTTGGCGAGG TCATGTGCCG GATCACCACG GTCGTTTTCT 420
104 ACGGCAACAT GTACTGCGCT ANNNTCCTGA TCCTCACCTG CATGGGCATC AACCGCTACC 480
105 TGGCCACGGC TCACCCTTTC ACATACCAGA AGCTGCCCAA ACGCAGCTTC TCCATGCTCA 540
106 TGTGTGGCAT GGTGTGGGTC ATGGTTTTCT TATACATGCT GCCCTTTGTC ATCCNNNAAG 600
107 CAGGAGTACC ACCTCGTCCA CTCCGAGATC ACCACCTGCC ACGATGTCGT CGACGCGTGC 660
108 GANTCCCAT CATCCTTCCG ATTCTACTAC TTCGTCTCCT TAGCATTCTT TGGGTTCTCT 720
109 ATCCCGTTTG TGATCATCAT CTTCTGTTC ACGACTCTCA TCCACAACT TAAATCAAAA 780
110 GATCNGATAT GGCTGGGCTA CATCAAGGCC GTCCTCCTCA TCCTTGTAAG TTTACCATC 840
111 TGCTTCCCCC CCACCAAGNN NNNNGATATC TGGGAAGACG TACATGCTTG GCTGACTTGT 900
112 GCATGGCACC ATCAGCTCAA TTTTAAATTT TTTAATTTTA ATTTAATTTA ATTTTATGTT 960
113 TTTGAGACAG AGCCTCACTG TGTAGTCCTG GCTGGCCTGG CTGGTTCTCT ATTTAGACCA 1020
114 GGTTAGCCTT GAACTCACAG AGATCTGCCT GCTTCTGCCT CCCAAGTGCT GGGTTCAACC 1080
115 AGGTCTGGCA AGCGCTCCAT TTTTCAGCTC CTCTGCAACA GTGC 1124

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 5, 386, 394
- (D) OTHER INFORMATION: Xaa = stop

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

131 invalid
132
133 Thr Leu Tyr Thr Xaa Gln His Pro Val Ala Gly Ser Gln Asp Ile Lys
134 1 5 10 15
135 Met Lys Ile Leu Ile Leu Val Ala Ala Gly Leu Leu Phe Leu Pro Val
136 20 25 30
137 Thr Val Cys Gln Ser Gly Ile Asn Val Ser Asp Asn Ser Ala Lys Pro
138 35 40 45
139 Thr Leu Thr Ile Lys Ser Phe Asn Gly Gly Pro Gln Asn Thr Phe Glu
140 50 55 60
141 Glu Phe Pro Leu Ser Asp Ile Glu Gly Trp Thr Gly Ala Thr Thr Thr
142 65 70 75 80
143 Ile Lys Ala Glu Cys Pro Glu Asp Ser Ile Ser Thr Leu His Val Asn
144 85 90 95
145 Asn Ala Thr Ile Gly Tyr Leu Arg Ser Ser Leu Ser Thr Gln Val Ile
146 100 105 110
147 Pro Ala Ile Tyr Ile Leu Leu Phe Val Val Gly Val Pro Ser Asn Ile
148 115 120 125
149 Val Thr Leu Trp Lys Leu Ser Leu Arg Thr Lys Ser Ile Ser Leu Val
150 130 135 140
151 Ile Phe His Thr Asn Leu Ala Ile Ala Asp Leu Leu Phe Cys Val Thr
152 145 150 155 160

```

*This error appears in
Seq. 6, too.*

rep. 4, too

*Xaa can only represent an
amino acid. A group of
4 or more amino acids*

*following a
stop codon
must
be shown as
a separate
sequence,
with a
different
sequence.*

*Identification
number, and
amino acids*

*Also, the response to (iii) NUMBER OF SEQUENCES: MUST accommodate
numbered accordingly.*

RAW SEQUENCE LISTING PATENT APPLICATION US/09/208,629

DATE: 12/10/2000
TIME: 03:01:31

INPUT SET: S36189.raw

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153  Leu Pro Phe Lys Ile Ala Tyr His Leu Asn Gly Asn Asn Trp Val Phe
154                      165                      170                      175
155  Gly Glu Val Met Cys Arg Ile Thr Thr Val Val Phe Tyr Gly Asn Met
156                      180                      185                      190
157  Tyr Cys Ala Ile Leu Ile Leu Thr Cys Met Gly Ile Asn Arg Tyr Leu
158                      195                      200                      205
159  Ala Thr Ala His Pro Phe Thr Tyr Gln Lys Leu Pro Lys Arg Ser Phe
160                      210                      215                      220
161  Ser Leu Leu Met Cys Gly Ile Val Trp Val Met Val Phe Leu Tyr Met
162                      225                      230                      235                      240
163  Leu Pro Phe Val Ile Leu Lys Gln Glu Tyr His Leu Val His Ser Glu
164                      245                      250                      255
165  Ile Thr Thr Cys His Asp Val Val Asp Ala Cys Glu Ser Pro Ser Ser
166                      260                      265                      270
167  Phe Arg Phe Tyr Tyr Phe Val Ser Leu Ala Phe Phe Gly Phe Leu Ile
168                      275                      280                      285
169  Pro Phe Val Ile Ile Ile Phe Cys Tyr Thr Thr Leu Ile His Lys Leu
170                      290                      295                      300
171  Lys Ser Lys Asp Arg Ile Trp Leu Gly Tyr Ile Lys Ala Val Leu Leu
172                      305                      310                      315                      320
173  Ile Leu Val Ile Phe Thr Ile Cys Phe Ala Pro Thr Asn Ile Ile Leu
174                      325                      330                      335
175  Val Ile His His Ala Asn Tyr Tyr Tyr His Asn Thr Asp Ser Leu Tyr
176                      340                      345                      350
177  Phe Met Tyr Leu Ile Ala Leu Cys Leu Gly Ser Leu Asn Ser Cys Leu
178                      355                      360                      365
179  Asp Pro Phe Leu Tyr Phe Val Met Ser Lys Val Val Asp Gln Leu Asn
180                      370                      375                      380
181  Pro Xaa Ser Ala Met Ala Arg Pro Leu Xaa Arg Pro Arg Arg Asp Ile
182                      385                      390                      395                      400
183  Trp Glu Asp Ile His Ala Trp
184                      405
185

```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

197
198  TGCTCCATGA TTTTACAGAT TTCATAACGT TTAAGAGACG GGA CTCAGGT CATCAAAATG      60
199  AAAGCCCTCA TCCTTGACAGC TGCTGGCCTC CTGCTTCTGT TGCCCACTTT TTGTCAGAGT      120
200  GGCATGGAAA ATGATACAAA CAACTTGGCA AAGCCAACCT TACCCATTAA GACCTTTCGT      180
201  GGAGCTCCCC CAAATTCTTT TGAAGAGTTC CCCTTTTCTG CCTTGGAAGG CTGGACAGGA      240
202  GCCACGATTA CTGTAAAAAT TAAGTGCCTT GAAGAAAGTG CTTACATCTT CCATGTGAAA      300
203  AATGCTACCA TGGGGTACCT GACCAGCTCC TTAAGTACTA AACTGATACC TGCCATCTAC      360
204  CTCCTGGTGT TTGTAGTTGG TGTCCCGGCC AATGCTGTGA CCCTGTGGAT GCTTTTCTTC      420
205  AGGACCAGAT CCATCTGTAC CACTGTATTG TACACCAACC TGGCCATTGC AGATTTTCTT      480

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/208,629DATE: 12/10/2000
TIME: 03:01:31

INPUT SET: S36189.raw

206	TTTTGTGTTA	CATTGCCCTT	TAAGATAGCT	TATCATCTCA	ATGGGAACAA	CTGGGTATTT	540
207	GGAGAGGTCC	TGTGCCGGGC	CACCACAGTC	ATCTTCTATG	GCAACATGTA	CTGCTCCATT	600
208	CTGCTCCTTG	CCTGCATCAG	CATCAACCGC	TACCTGGCCA	TCGTCCATCC	TTTCACCTAC	660
209	CGGGGCCTGC	CCAAGCACAC	CTATGCCTTG	GTAACATGTG	GA CTGGTGTG	GGCAACAGTT	720
210	TTCTTATATA	TGCTGCCATT	TTTCATACTG	AAGCAGGAAT	ATTATCTTGT	TCAGCCAGAC	780
211	ATCACCACCT	GCCATGATGT	TCACAACACT	TGCGAGTCCT	CATCTCCCTT	CCAACCTCTAT	840
212	TACTTCATCT	CCTTGGCATT	CTTTGGATTG	TTAATTCCAT	TTGTGCTTAT	CATCTACTGC	900
213	TATGCAGCCA	TCATCCGGAC	ACTTAATGCA	TACGATCATA	GATGGTTGTG	GTATGTAAAG	960
214	GCGAGTCTCC	TCATCCTTGT	GATTTTTTACC	ATTTGCTTTG	CTCCAAGCAA	TATTATTCTT	1020
215	ATTATTCACC	ATGCTAACTA	CTACTACAAC	AACACTGATG	GCTTATATTT	TATATATCTC	1080
216	ATAGCTTTGT	GCCTGGGTAG	TCTTAATAGT	TGCTTAGATC	CATTCCCTTA	TTTTCTCATG	1140
217	TCAAAAACCA	GAAATCACTC	CACTGCTTAC	CTTACAAAT	AGTGAAATGA	TCTTAGAGAA	1200
218	CAAGGACAGC	CATCACAGAG	AACG				1224

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

231							
232	ACAGGCATGG	AAAATGATAC	AAACAACCTTG	GCAAAGCCAA	CCTTACCCAT	TAAGACCTTT	60
233	CGTGGAGCTC	CCCCAAATTC	TTTTGAAGAG	TTCCCCTTTT	CTGCCTTGGA	AGGCTGGACA	120
234	GGAGCCACGA	TTACTGTAAA	AATTAAGTGC	CCTGAAGAAA	GTGCTTCACA	TCTCCATGTG	180
235	AAAAATGCTA	CCATGGGGTA	CCTGACCAGC	TCCTTAAGTA	CTAAACTGAT	ACCTGCCATC	240
236	TACCTCCTGG	TGTTTGTAGT	TGGTGTCCCG	GCCAATGCTG	TGACCCTGTG	GATGCTTTTC	300
237	TTCAGGACCA	GATCCATCTG	TACCACTGTA	TTCTACACCA	ACCTGGCCAT	TGCAGATTTT	360
238	CTTTTTTTGTG	TTACATTGCC	CTTTAAGATA	GCTTATCATC	TCAATGGGAA	CAACTGGGTA	420
239	TTTGGAGAGG	TCCTGTGCCG	GGCCACCACA	GTCACTTTCT	ATGGCAACAT	GTACTGCTCC	480
240	ATTCTGCTCC	TTGCCTGCAT	CAGCATCAAC	CGCTACCTGG	CCATCGTCCA	TCCTTTCCACC	540
241	TACCGGGGCC	TGCCCAAGCA	CACCTATGCC	TTGGTAACAT	GTGGACTGGT	GTGGGCAACA	600
242	GTTTTCTTAT	ATATGCTGCC	ATTTTTTATA	CTGAAGCAGG	AATATTATCT	TGTTTCAGCCA	660
243	GACATCACCA	CCTGCCATGA	TGTTCAACAAC	ACTTGCGAGT	CCTCATCTCC	CTTCCAACCTC	720
244	TATTACTTCA	TCTCCTTGCC	ATTCTTTGGA	TTCTTAATTC	CATTTGTGCT	TATCATCTAC	780
245	TGCTATGCAG	CCATCATCCG	GACACTTAAT	GCATACGATC	ATAGATGGTT	GTGGTATGTT	840
246	AAGGCGAGTC	TCCTCATCCT	TGTGATTTTT	ACCATTGCTT	TTGCTCCAAG	CAATATTATT	900
247	CTTATTATTC	ACCATGCTAA	CTACTACTAC	AACAACACTG	ATGGCTTATA	TTTTATATAT	960
248	CTCATAGCTT	TGTGCTGGG	TAGTCTTAAT	AGTTGCTTAG	ATCCATTCCCT	TTATTTTCTC	1020
249	ATGTCAAAAA	CCAGAAATCA	CTCCACTGCT	TACCTTACAA	AATAGTGAAA	TGATCTTAGA	1080
250	GAACAAGGAC	AGCCATCACA	GA				1102

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

PAGE: 1

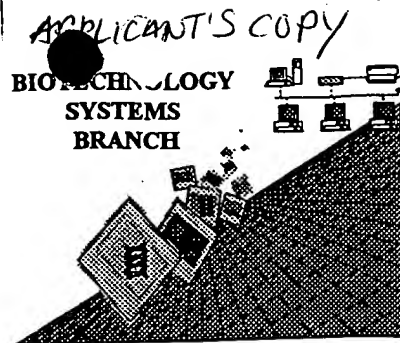
SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/208,629

DATE: 12/10/2000
TIME: 03:01:31

INPUT SET: S36189.raw

Line	Error	Original Text
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Pak



#8

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/208,629

Source: 1646

Date Processed by STIC: 7/10/2000

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JUL 28 2000

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER,
703-308-4212.**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:**

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

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1646

RAW SEQUENCE LISTING DATE: 07/10/2000
 PATENT APPLICATION: US/09/208,629 TIME: 12:18:59

Input Set : A:\22000-20603.10-Seq.txt
 Output Set: N:\CRF3\07102000\I208629.raw

SEQUENCE LISTING

C--> 5 (1) GENERAL INFORMATION:
 7 (i) APPLICANT: Coughlin, Shaun
 8 Ishihari, Hiroaki
 9 Connolly, Andrew
 C--> 11 (ii) TITLE OF INVENTION: Protease Activated Receptor
 12 3 and Uses Thereof
 14 (iii) NUMBER OF SEQUENCES: 23
 16 (iv) CORRESPONDENCE ADDRESS:
 17 (A) ADDRESSEE: MORRISON & FOERSTER
 18 (B) STREET: 755 Page Mill Road
 19 (C) CITY: Palo Alto
 20 (D) STATE: California
 21 (E) COUNTRY: USA
 22 (F) ZIP: 94304-1018
 24 (v) COMPUTER READABLE FORM:
 25 (A) MEDIUM TYPE: Diskette
 26 (B) COMPUTER: IBM Compatible
 27 (C) OPERATING SYSTEM: DOS
 28 (D) SOFTWARE: FastSEQ for Windows Version 2.0
 C--> 30 (vi) CURRENT APPLICATION DATA:
 C--> 31 (A) APPLICATION NUMBER: US/09/208,629
 C--> 32 (B) FILING DATE: 22-Jun-2000
 33 (C) CLASSIFICATION:
 35 (vii) PRIOR APPLICATION DATA:
 36 (A) APPLICATION NUMBER: 08/742,440
 37 (B) FILING DATE: 30-OCT-1996
 39 (viii) ATTORNEY/AGENT INFORMATION:
 40 (A) NAME: Catherine M. Polizzi
 41 (B) REGISTRATION NUMBER: 40,130
 42 (C) REFERENCE/DOCKET NUMBER: 22000-20604.00
 44 (ix) TELECOMMUNICATION INFORMATION:
 45 (A) TELEPHONE: (650) 813-5600
 46 (B) TELEFAX: (650) 494-0792
 47 (C) TELEX: 706141

Does Not Comply
 Corrected Diskette Needed

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ERRORED SEQUENCES

464 (2) INFORMATION FOR SEQ ID NO: 10:
 466 (i) SEQUENCE CHARACTERISTICS:
 467 (A) LENGTH: 29 base pairs
 468 (B) TYPE: nucleic acid
 469 (C) STRANDEDNESS: double
 470 (D) TOPOLOGY: linear
 472 (ii) MOLECULE TYPE: cDNA
 473 (ix) FEATURE:

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/208,629

DATE: 07/10/2000
 TIME: 12:18:59

Input Set : A:\22000-20603.10-Seq.txt
 Output Set: N:\CRF3\07102000\I208629.raw

```

481      (A) NAME/KEY: Other
476      (B) LOCATION: 1...29
477      (D) OTHER INFORMATION: N=Inosine at residues 3, 12, 18, 21, and 24
486      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
E--> 488  GINTACATGC TNMACYTNGC NNTNGCNGA
490      (2) INFORMATION FOR SEQ ID NO: 11:
492      (i) SEQUENCE CHARACTERISTICS:
493          (A) LENGTH: 26 base pairs
494          (B) TYPE: nucleic acid
495          (C) STRANDEDNESS: double
496          (D) TOPOLOGY: linear
498      (ii) MOLECULE TYPE: cDNA
499      (ix) FEATURE:
500          (A) NAME/KEY: Other
501          (B) LOCATION: 6...21
502          (D) OTHER INFORMATION: N=Inosine at residue 6, 9, 12, 15, and 21
504      (ix) FEATURE:
505          (A) NAME/KEY: Other
506          (B) LOCATION: 24
507          (D) OTHER INFORMATION: N=A or C or G or T at residue 24
509      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
E--> 511  GGATANACNA CNGCNADRWA NCKBTC
687      (2) INFORMATION FOR SEQ ID NO: 23:
689      (i) SEQUENCE CHARACTERISTICS:
690          (A) LENGTH: 9 amino acids
691          (B) TYPE: amino acid
692          (C) STRANDEDNESS: single
693          (D) TOPOLOGY: linear
696      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:
698      Thr Phe Arg Gly Ala Pro Pro Asn Ser
699      1 5
E--> 700  1
E--> 701  1

```

*29 ← insert cumulative base
 noted at end of each
 line*

B is at location 24

26 ← insert

delete at end of file

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/208,629

DATE: 07/10/2000

TIME: 12:19:00

Input Set : A:\22000-20603.10-Seq.txt

Output Set: N:\CRF3\07102000\I208629.raw

L:5 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:11 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:30 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]
L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:94 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=2, Value={ }
L:128 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:128 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=3, Value={Xaa = stop}
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:262 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:262 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=6, Value={Xaa = stop}
L:266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:488 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:488 M:333 E: Wrong sequence grouping, Amino acids not in groups:
L:488 M:204 E: No. of Bases differ, LENGTH:Input:29 Counted:0 SEQ:10
L:511 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:511 M:333 E: Wrong sequence grouping, Amino acids not in groups:
L:511 M:204 E: No. of Bases differ, LENGTH:Input:26 Counted:0 SEQ:11
L:648 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=20, Value={ }
L:650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:665 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=21, Value={ }
L:667 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:700 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
M:332 Repeated in SeqNo=23

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